

Open Source Software

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For more information regarding how to access software from Los Alamos, contact the <u>Software</u> Team.

- <u>brulilo</u>, <u>Version 0.x</u>brulilo is a Python package for building and evolving thermonuclear reaction networks.
- Byfl: Compiler-based Application Analysis Byfl is a productivity tool that helps computational scientists analyze their code for accelerator-friendly and acceleratorunfriendly constructs.
- <u>CLAMR (Compute Language Adaptive Mesh Refinement)</u> CLAMR is being developed as a DOE mini-app, one of several applications being developed to help prepare for the Exascale class of heterogeneous hardware platforms.
- CODY: Continuum Dynamics Evaluation and Test SuiteCODY is a development framework and suite of small applications, or "mini-apps", characteristic of continuum dynamics applications that will be used for research in new programming models, software environments, and the evaluation of new computer architectures.
- coNCePTuaL -- A Network Correctness and Performance Testing LanguagecoNCePTuaL
 is a tool designed to facilitate rapidly generating programs that measure the performance
 and/or test the correctness of networks and network protocol layers
- db, Version 0.2.xA set of programs and utilities for generating and manipulating data files in TSV (tab-separated value) or JSON format.
- Genome Majority Vote The pipeline runs PRODIGAL gene predictions on all genomes, runs pan-reciprocal BLAST, and identifies ortholog sets.
- HASH v.1.xDescribed in the journal article and presentations, "Hash-Based Algorithms for Discretized Data," hash algorithms are to be distributed for starting points for optimization efforts.
- HASH v.2.xEnhancements to hash version 1.x, with compact hash techniques and described in the journal article, "Compact Hash Algorithms for Computational Meshes."
- HILO: Quasi Diffusion Accelerated Monte Carlo on Hybrid Architectures The Boltzmann transport equation provides high fidelity simulation of a diverse range of kinetic systems.
 We present a novel algorithm, Quasi-Diffusion Accelerated Monte Carlo (QDA-MC), which improves performance on heterogeneous CPU/GPU architectures.
- <u>LANL Go Suite</u> The LANL Go Suite is a collection of packages, libraries, utilities, and software patches related to Google's Go programming language. The LANL Go Suite largely takes a high-performance computing angle to Go.
- <u>Libparty</u>, <u>Version 1.x</u>General particle library designed to run on next-generation hardware such as MICs and GPUs
- Model Analysis ToolKit (MATK), Version 0MATK provides basic functionality to facilitate model analysis within the Python computational environment.

- McPhDMcPhD is a research code designed to explore the applications of the Haskell programming language to Monte Carlo algorithms.
- MeGAMerge, Version 1.0A novel method of merging of multiple genomic assembly or long read data sources for assembly.
- mFUSE: Function Sequencer for MATLAB, Version 0.1.00mFUSE: Function Sequencer for MATLAB is a Java based graphical user interface for use with MATLAB.
- Multi-Dimensional Hashed Indexed Metadata (MDHIM) System The MDHIM software is a revolutionary new software tool that performs more than a billion key/value inserts per second into a globally ordered key space.
- NuTNuT is a Monte Carlo neutrino transport code for astrophysics simulations.
- <u>PENNANT</u>PENNANT is a mini-app intended for use in advanced architecture research.
- PISTON (Portable Data Parallel Visualization and Analysis) A Portable Cross-Platform Data-Parallel Visualization and Analysis Library
- <u>POSTMAX</u>, <u>Version 2.0</u>POSTMAX is a small program developed to statistically analyze MACCS2 output to determine a 95th percentile value for atmospheric dispersion (x/Q) as a function of weather data and site boundary distance.
- PROSIG, Version 1.xPROSIG designs nucleic acid-based assays that detect specified target sequences and do not detect specific non-target sequences.
- <u>PyFEHM</u>PyFEHM is a set of Python libraries designed to be used with the LANL simulation code FEHM.
- <u>PyVXI-11</u>, <u>Version 1.0</u>PyVXI-11 is a Python extension to interface with electronics laboratory equipment such as oscilloscopes, network and spectrum analyzes, multimeters, etc., using the standard SCPI language and TCP/IP.
- <u>ramdisk</u>, <u>Version 0.x</u>The intent of the software is eventually to become a middleware library to provide a cross platform interface for creating and managing a ramdisk.
- <u>Seismoacoustic Software</u>Addressing local and regional-scale seismological and infrasound problems through a combination of theory, data analysis and field deployments in support of United States treaty/explosion monitoring.
- <u>SHMTools</u>SHMTools is a MATLAB package that facilitates the construction of structural health monitoring (SHM) processes.
- <u>SNAP:SN (Discrete Ordinates) Application Proxy</u>SNAP serves as a proxy application to model the performance of a modern discrete ordinates neutral particle transport application.
- STONIX, Version 0.xSTONIX is a program for configuring UNIX and Linux computer operating systems.
- <u>ThermonucleotideBLAST</u>ThermonucleotideBLAST is a software program for searching a target database of nucleic acid sequences using an assay specific query.
- tsk_get_filestsk_get_files is a script that uses "The Sleuth Kit" commands "fls" and "icat" to rebuild a file structure from a disk image.
- <u>Total-Variation Regularized Numerical Differentiation (TVDiff), Version 1.0</u>This code computes the derivative of a function specified by noisy data using regularization to suppress noise amplification.
- Two Sample T-Test for Comparing Genetic Sequence Diversity Given two samples of sequences the program performs a t-test to see whether the two mean genetic distances are significantly different.
- <u>Zenoss</u>The HPC monitoring project goal was to extend upon the Zenoss core produce to provide large scale system monitoring, data collection and reporting, and root cause isolation for high-performance computers and isolated infrastructure.

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